

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: VETIGEN
 (B) STREET: 21 rue Sébastien Mercier
 (C) CITY: PARIS
 (E) COUNTRY: FRANCE
 (F) POSTAL CODE (ZIP): 75015

(A) NAME: LENZEN Gerlinde
 (B) STREET: 55 rue des Cévennes
 (C) CITY: PARIS
 (E) COUNTRY: FRANCE
 (F) POSTAL CODE (ZIP): 75015

(A) NAME: STROSBERG Arthur Donny
 (B) STREET: 66 rue de Javel
 (C) CITY: PARIS
 (E) COUNTRY: FRANCE
 (F) POSTAL CODE (ZIP): 75015

(A) NAME: SUGASAWA Toshinari
 (B) STREET: 9-12-507 Miyano-cho, Takatsuki-shi
 (C) CITY: OSAKA
 (E) COUNTRY: JAPON
 (F) POSTAL CODE (ZIP): 569

(A) NAME: MOROOKA Shigeako
 (B) STREET: 4-78 nishi-3, Seiwadai, Kawanishi-shi
 (C) CITY: HYOGO
 (E) COUNTRY: JAPON
 (F) POSTAL CODE (ZIP): 666-01

(ii) TITLE OF INVENTION: NON-ADRENERGIC RECEPTOR AND ITS APPLICATIONS.

(iii) NUMBER OF SEQUENCES: 14

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met	Tyr	Ile	Asp	Asp	Leu	Pro	Ile	Trp	Gly	Ile	Val	Gly	Glu	Ala	Asp
1					5				10					15	
Glu	Asn	Gly	Glu	Asp	Tyr	Tyr	Leu	Trp	Thr	Tyr	Lys	Lys	Leu	Glu	Ile
		20						25					30		
Gly	Phe	Asn	Gly	Asn	Arg	Ile	Val	Asp	Val	Asn	Leu	Thr	Ser	Glu	Gly
		35					40					45			

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Lys Val Lys Leu Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val
 50 55 60
 Lys Trp Lys Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr
 65 70 75 80
 Leu Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe
 85 90 95
 Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile
 100 105 110
 Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu
 115 120 125
 Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys
 130 135 140
 Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe
 145 150 155 160
 Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile
 165 170 175
 Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser
 180 185 190
 Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn
 195 200 205
 Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp
 210 215 220
 Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys
 225 230 235 240
 Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser
 245 250 255
 Arg Ala Ile Pro Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe
 260 265 270
 Phe Val Ile Leu Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn
 275 280 285
 Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg
 290 295 300
 Pro Ile Pro Glu Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys
 305 310 315 320
 Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe
 325 330 335
 Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe
 340 345 350
 Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr
 355 360 365
 Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln
 370 375 380
 Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met
 385 390 395 400
 Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe
 405 410 415

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Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu
420 425 430

Gly Ile Met Cys Gly Ala Ile
435

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGTACATAG ATGATTTACC AATATGGGGT ATTGTTGGTG AGGCTGATGA AAATGGAGAA 60
GATTACTATC TTTGGACCTA TAAAAACTT GAAATAGGTT TTAATGGAAA TCGAATTGTT 120
GATGTTAATC TAACTAGTGA AGGAAAGGTG AAAGTGGTTC CAAATACTAA AATCCAGATG 180
TCATATTCAG TAAATGGAA AAAGTCAGAT GTGAAATTG AAGATCGATT TGACAAATAT 240
CTTGATCCGT CCTTTTTTCA ACATCGGATT CATTGGTTTT CAATTTTCAA CTCCTTCATG 300
ATGGTGATCT TCTTGGTGGG CTTAGTTTCA ATGATTTTAA TGAGAACATT AAGAAAAGAT 360
TATGCTCGGT ACAGTAAAGA GGAAGAAATG GATGATATGG ATAGAGACCT AGGAGATGAA 420
TATGGATGGA AACAGGTGCA TGGAGATGTA TTTAGACCAT CAAGTCACCC ACTGATATTT 480
TCCTCTCTGA TTGGTTCTGG ATGTCAGATA TTGCTGTGT CTCTCATCGT TATTATTGTT 540
GCAATGATAG AAGATTTATA TACTGAGAGG GGATCAATGC TCAGTACAGC CATATTTGTC 600
TATGCTGCTA CGTCTCCAGT GAATGGTTAT TTTGGAGGAA GTCTGTATGC TAGACAAGGA 660
GGAAGGAGAT GGATAAAGCA GATGTTTATT GGGGCATTCC TTATCCCAGC TATGGTGTGT 720
GGCACTGCCT TCTTCATCAA TTTCATAGCC ATTTATTACC ATGCTTCAAG AGCCATTCCCT 780
TTTGGAACAA TGGTGGCCGT TTGTTGCATC TGTTTTTTTG TTATTCTTCC TCTAAATCTT 840
GTTGGTACAA TACTTGGCCG AAATCTGTCA GGTGAGCCCA ACTTTCCTTG TCGTGTCAAT 900
GCTGTGCCTC GTCCTATACC GGAGAAAAAA TGGTTCATGG AGCCTGCGGT TATTGTTTGC 960
CTGGGTGGAA TTTTACCTTT TGGTTCAATC TTTATTGAAA TGTATTTTCA CTTCACGTCT 1020
TTCTGGGCAT ATAAGATCTA TTATGTCTAT GGCTTCATGA TGCTGGTGCT GGTATCCTG 1080
TGCATTGTGA CTGTCTGTGT GACTATTGTG TGCACATATT TTCTACTAAA TGCAGAAGAT 1140
TACCGGTGGC AATGGACAAG TTTTCTCTCT GCTGCATCAA CTGCAATCTA TGTTTACATG 1200
TATTCTTTT ACTACTATTT TTCAAACA AAGATGTATG GCTTATTTCA AACATCATTT 1260
TACTTTGGAT ATATGGCGGT ATTTAGCACA GCCTTGGGGA TAATGTGTGG AGCGATT 1317

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 965 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGATGTCAT ATTCAGTAA ATGAAAAAG TCAGATGTGA AATTTGAAGA TCGATTTGAC 60
 AAATATCTTG ATCCGTCCTT TTTTCAACAT CGGATTCATT GGTTTTCAAT TTCAACTCC 120
 TTCATGATGG TGATCTTCTT GGTGGGCTTA GTTTCAATGA TTTTAATGAG AACATTAAGA 180
 AAAGATTATG CTCGGTACAG TAAAGAGGAA GAAATGGATG ATATGGATAG AGACCTAGGA 240
 GATGAATATG GATGGAAACA GGTGCATGGA GATGTATTTA GACCATCAAG TCACCCACTG 300
 ATATTTTCCT CTCTGATTGG TTCTGGATGT CAGATATTTG CTGTGTCTCT CATCGTTATT 360
 ATTGTTGCAA TGATAGAAGA TTTATATACT GAGAGGGGAT CAATGCTCAG TACAGCCATA 420
 TTTGTCTATG CTGCTACGTC TCCAGTGAAT GGTTATTTTA GAGGAAGTCT GTATGCTAGA 480
 CAAGGAGGAA GGAGATGGAT AAAGCAGATG TTTATTGGGG CATTCCTTAT CCCAGCTATG 540
 GTGTGTGGCA CTGCCTTCTT CATCAATTTT ATAGCCATTT ATTACCATGC TTCAAGAGCC 600
 ATTCCTTTTG GAACAATGGT GGCCGTTTGT TGCATCTGTT TTTTGTAT TCTTCCTCTA 660
 AATCTTGTG GTACAATACT TGGCCGAAAT CTGTCAGGTC AGCCCAACTT TCCTTGTCGT 720
 GTCAATGCTG TGCCTCGTCC TATACCGGAG AAAAAATGGT TCATGGAGCC TGCGGTTATT 780
 GTTGCCTGG GTGGAATTTT ACCTTTTGGT TCAATCTTTA TTGAAATGTA TTTCATCTTC 840
 ACGTCTTTCT GGGCATATAA GATCTATTAT GTCTATGCT TCATGATGCT GGTGCTGGTT 900
 ATCCTGTGCA TTGTGACTGT CTGTGTGACT ATTGTGTGCA CATATTTTCT ACTAAATGCA 960
 GAAGA 965

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCAGTAAAAT GGAAAAAGTC AGATGTGAAA TTTGAAGATC GATTGACAA ATATCTTGAT 60
 CCGTCCTTTT TTCAACATCG GATTCATTGG TTTTCAATTT TCAACTCCTT CATGATGGTG 120
 ATCTTCTTGG TGGGCTTAGT TTCAATGATT TTAATGAGAA CATTAGAAA AGATTATGCT 180
 CGGTACAGTA AAGAGGAAGA AATGGATGAT ATGGATAGAG ACCTAGGAGA TGAATATGGA 240
 TGGAAACAGG TGCATGGAGA TGTATTTAGA CCATCAAGTC ACCCA 285

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(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe Asn
 1 5 10 15
 Ser

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp Pro Xaa Phe Phe Gln His Arg Ile His Val Phe Ser Ile Phe Asn
 1 5 10 15
 His

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "AMORCE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCAGTAAAAT GGAAAAAGTC

20

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "AMORCE"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TGGGTGACTT GATGGTCTAA

20

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "AMORCE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCTGTGTCTC TCATCGTTA

19

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "AMORCE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CCATCCATAT TCATCTCCTA

20

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "AMORCE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGGTATAGGA CGAGGCACAG C

21

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "AMORCE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ACTGAATATG ACATCTGG

18

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(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) ~~FEATURE:~~

(A) NAME/KEY: CDS
(B) LOCATION: 3..1730

CC	GCC	GCG	CTG	TGG	CTG	CTG	CTG	CTG	CTG	CCC	CGG	ACC	CGG	GCG		47
	Ala	Ala	Leu	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Arg	Thr	Arg	Ala		
	1				5				10					15		
GAC	GAG	CAC	GAA	CAC	ACG	TAT	CAA	GAT	AAA	GAG	GAA	GTT	GTC	TTA	TGG	95
Asp	Glu	His	Glu	His	Thr	Tyr	Gln	Asp	Lys	Glu	Glu	Val	Val	Leu	Trp	
				20					25					30		
ATG	AAT	ACT	GTT	GGG	CCC	TAC	CAT	AAT	CGT	CAA	GAA	ACA	TAT	AAG	TAC	143
Met	Asn	Thr	Val	Gly	Pro	Tyr	His	Asn	Arg	Gln	Glu	Thr	Tyr	Lys	Tyr	
			35					40					45			
TTT	TCA	CTT	CCA	TTC	TGT	GTG	GGG	TCA	AAA	AAA	AGT	ATC	AGT	CAT	TAC	191
Phe	Ser	Leu	Pro	Phe	Cys	Val	Gly	Ser	Lys	Lys	Ser	Ile	Ser	His	Tyr	
		50				55						60				
CAT	GAA	ACT	CTG	GGA	GAA	GCA	CTT	CAA	GGG	GTT	GAA	TTG	GAA	TTT	AGT	239
His	Glu	Thr	Leu	Gly	Glu	Ala	Leu	Gln	Gly	Val	Glu	Leu	Glu	Phe	Ser	
	65					70				75						
GGT	CTG	GAT	ATT	AAA	TTT	AAA	GAT	GAT	GTG	ATG	CCA	GCC	ACT	TAC	TGT	287
Gly	Leu	Asp	Ile	Lys	Phe	Lys	Asp	Asp	Val	Met	Pro	Ala	Thr	Tyr	Cys	
80				85					90						95	
GAA	ATT	GAT	TTA	GAT	AAA	GAA	AAG	AGA	GAT	GCA	TTT	GTA	TAT	GCC	ATA	335
Glu	Ile	Asp	Leu	Asp	Lys	Glu	Lys	Arg	Asp	Ala	Phe	Val	Tyr	Ala	Ile	
				100				105						110		
AAA	AAT	CAT	TAC	TGG	TAC	CAG	ATG	TAC	ATA	GAT	GAT	TTA	CCA	ATA	TGG	383
Lys	Asn	His	Tyr	Trp	Tyr	Gln	Met	Tyr	Ile	Asp	Asp	Leu	Pro	Ile	Trp	
			115					120					125			
GGT	ATT	GTT	GGT	GAG	GCT	GAT	GAA	AAT	GGA	GAA	GAT	TAC	TAT	CTT	TGG	431
Gly	Ile	Val	Gly	Glu	Ala	Asp	Glu	Asn	Gly	Glu	Asp	Tyr	Tyr	Leu	Trp	
	130					135						140				
ACC	TAT	AAA	AAA	CTT	GAA	ATA	GGT	TTT	AAT	GGA	AAT	CGA	ATT	GTT	GAT	479
Thr	Tyr	Lys	Lys	Leu	Glu	Ile	Gly	Phe	Asn	Gly	Asn	Arg	Ile	Val	Asp	
	145					150				155						
GTT	AAT	CTA	ACT	AGT	GAA	GGA	AAG	GTG	AAA	CTG	GTT	CCA	AAT	ACT	AAA	527
Val	Asn	Leu	Thr	Ser	Glu	Gly	Lys	Val	Lys	Leu	Val	Pro	Asn	Thr	Lys	
160					165					170					175	
ATC	CAG	ATG	TCA	TAT	TCA	GTA	AAA	TGG	AAA	AAG	TCA	GAT	GTG	AAA	TTT	575
Ile	Gln	Met	Ser	Tyr	Ser	Val	Lys	Trp	Lys	Lys	Ser	Asp	Val	Lys	Phe	
				180				185						190		
GAA	GAT	CGA	TTT	GAC	AAA	TAT	CTT	GAT	CCG	TCC	TTT	TTT	CAA	CAT	CGG	623
Glu	Asp	Arg	Phe	Asp	Lys	Tyr	Leu	Asp	Pro	Ser	Phe	Phe	Gln	His	Arg	
			195					200					205			

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ATT GAT TGG TTT TCA ATT TTC AAC TCC TTC ATG ATG GTG ATC TTC TTG Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu 210 215 220	671
GTG GGC TTA GTT TCA ATG ATT TTA ATG AGA ACA TTA AGA AAA GAT TAT Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr 225 230 235	719
GCT CGG TAC AGT AAA GAG GAA GAA ATG GAT GAT ATG GAT AGA GAC CTA Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu 240 245 250 255	767
GGA GAT GAA TAT GGA TGG AAA CAG GTG CAT GGA GAT GTA TTT AGA CCA Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro 260 265 270	815
TCA AGT CAC CCA CTG ATA TTT TCC TCT CTG ATT GGT TCT GGA TGT CAG Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln 275 280 285	863
ATA TTT GCT GTG TCT CTC ATC GTT ATT ATT GTT GCA ATG ATA GAA GAT Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp 290 295 300	911
TTA TAT ACT GAG AGG GGA TCA ATG CTC AGT ACA GCC ATA TTT GTC TAT Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr 305 310 315	959
GCT GCT ACG TCT CCA GTG AAT GGT TAT TTT GGA GGA AGT CTG TAT GCT Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala 320 325 330 335	1007
AGA CAA GGA GGA AGG AGA TGG ATA AAG CAG ATG TTT ATT GGG GCA TTC Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe 340 345 350	1055
CTT ATC CCA GCT ATG GTG TGT GGC ACT GCC TTC TTC ATC AAT TTC ATA Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile 355 360 365	1103
GCC ATT TAT TAC CAT GCT TCA AGA GCC ATT CCT TTT GGA ACA ATG GTG Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val 370 375 380	1151
GCC GTT TGT TGC ATC TGT TTT TTT GTT ATT CTT CCT CTA AAT CTT GTT Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val 385 390 395	1199
GGT ACA ATA CTT GGC CGA AAT CTG TCA GGT CAG CCC AAC TTT CCT TGT Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys 400 405 410 415	1247
CGT GTC AAT GCT GTG CCT CGT CCT ATA CCG GAG AAA AAA TGG TTC ATG Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met 420 425 430	1295
GAG CCT GCG GTT ATT GTT TGC CTG GGT GGA ATT TTA CCT TTT GGT TCA Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser 435 440 445	1343
ATC TTT ATT GAA ATG TAT TTC ATC TTC ACG TCT TTC TGG GCA TAT AAG Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys 450 455 460	1391
ATC TAT TAT GTC TAT GGC TTC ATG ATG CTG GTG CTG GTT ATC CTG TGC Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys 465 470 475	1439

ATT GTG ACT GTC TGT GTG ACT ATT GTG TGC ACA TAT TTT CTA CTA AAT 1487
 Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn
 480 485 490 495

GCA GAA GAT TAC CGG TGG CAA TGG ACA AGT TTT CTC TCT GCT GCA TCA 1535
 Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser
 500 505 510

ACT GCA ATC TAT GTT TAC ATG TAT TCC TTT TAC TAC TAT TTT TTC AAA 1583
 Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys
 515 520 525

ACA AAG ATG TAT GGC TTA TTT CAA ACA TCA TTT TAC TTT GGA TAT ATG 1631
 Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met
 530 535 540

GCG GTA TTT AGC ACA GCC TTG GGG ATA ATG TGT GGA GCG ATT GGT TAC 1679
 Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr
 545 550 555

ATG GGA ACA AGT GCC TTT GTC CGA AAA ATC TAT ACT AAT GTG AAA ATT 1727
 Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile
 560 565 570 575

GAC TAGAGACCCA AGAAAACCTG GAACTTTGGA TCAATTTCTT TTTCATAGGG 1780
 Asp

GTGGAACCTTG CACAGCAAAA 1800

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Ala Ala Leu Trp Leu Leu Leu Leu Leu Pro Arg Thr Arg Ala Asp
 1 5 10 15
 Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp Met
 20 25 30
 Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr Phe
 35 40 45
 Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr His
 50 55 60
 Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser Gly
 65 70 75 80
 Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys Glu
 85 90 95
 Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile Lys
 100 105 110
 Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly
 115 120 125
 Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr
 130 135 140
 Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp Val

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145 150 155 160
Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys Ile
165 170 175
Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe Glu
180 185 190
Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg Ile
195 200 205
His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu Val
210 215 220
Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala
225 230 235 240
Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu Gly
245 250 255
Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro Ser
260 265 270
Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile
275 280 285
Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp Leu
290 295 300
Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr Ala
305 310 315 320
Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg
325 330 335
Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe Leu
340 345 350
Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala
355 360 365
Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val Ala
370 375 380
Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val Gly
385 390 395 400
Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg
405 410 415
Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met Glu
420 425 430
Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile
435 440 445
Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile
450 455 460
Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile
465 470 475 480
Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala
485 490 495
Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr
500 505 510
Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr

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515

520

525

Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala
530 535 540

Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr Met
545 550 555 560

Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp
565 570 575

09319724-090899

MICROORGANISMS

Optional Sheet in connection with the microorganism referred to on page 5, line 25 of the description.

A. IDENTIFICATION OF DEPOSIT:

Further deposits are identified on an additional sheet. 7

Name of depository institution •

Collection Nationale de Cultures de Micro-organismes

Address of depository institution (including postal code and country) :

28 rue du Docteur Roux, 75724 PARIS CEDEX 15

Date of deposit:

December 10, 1996

Accession Number 6

I-1795

8. ADDITIONAL INDICATIONS: (leave blank if not applicable). This information is continued on a separate attached sheet.

"With regard to the nominations in which a European patent is applied for, until the publication of the mention of the grant of the European patent or until the date on which the application shall be refused or withdrawn or shall be deemed to be withdrawn, a sample of the deposited microorganism shall be available only by the issue of a sample to an expert nominated by the requester. (Rule 28.4) of the EPC)".

C. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE * (If the indications are not for all designated States)

EUROPE
CANADA
JAPAN
UNITED STATES OF AMERICA

D. SEPARATE FURNISHING OF INDICATIONS * (leave blank if not applicable)

The indications listed below will be submitted to the International Bureau later. (Specify the general nature of the indications e.g., "Accession Number of Deposit")

L. ☒ This sheet was received with the international application when filed (to be checked by the receiving Office)

(illegible signature)

~~DATA~~ ~~FA9GLE~~ (Authorized Officer)

☐ The date of receipt (from the applicant) by the International Bureau is:

was

(Authorized Officer)

(January 1985)

031274-03039